
Core transcriptional regulatory circuit controlled by the TAL1 complex in human T cell acute lymphoblastic leukemia.

Journal: Cancer Cell

Publication Year: 2012

Authors: Takaomi Sanda, Lee N Lawton, M Inmaculada Barrasa, Zi Peng Fan, Holger Kohlhammer, Alejandro Gutierrez, Wenxue Ma, Jessica Tatarek, Yebin Ahn, Michelle A Kelliher, Catriona H M Jamieson, Louis M Staudt, Richard A Young, A Thomas Look

PubMed link: 22897851

Funding Grants: Derivation and Characterization of Myeloproliferative Disorder Stem Cells from Human ES Cells, Derivation and Characterization of Cancer Stem Cells from Human ES Cells, Preclinical development of a pan Bcl2 inhibitor for cancer stem cell directed therapy

Public Summary:

The oncogenic transcription factor TAL1/SCL is aberrantly expressed in over 40% of cases of human T cell acute lymphoblastic leukemia (T-ALL), emphasizing its importance in the molecular pathogenesis of T-ALL. Here we identify the core transcriptional regulatory circuit controlled by TAL1 and its regulatory partners HEB, E2A, LMO1/2, GATA3, and RUNX1. We show that TAL1 forms a positive interconnected autoregulatory loop with GATA3 and RUNX1 and that the TAL1 complex directly activates the MYB oncogene, forming a positive feed-forward regulatory loop that reinforces and stabilizes the TAL1-regulated oncogenic program. One of the critical downstream targets in this circuitry is the TRIB2 gene, which is oppositely regulated by TAL1 and E2A/HEB and is essential for the survival of T-ALL cells.

Scientific Abstract:

The oncogenic transcription factor TAL1/SCL is aberrantly expressed in over 40% of cases of human T cell acute lymphoblastic leukemia (T-ALL), emphasizing its importance in the molecular pathogenesis of T-ALL. Here we identify the core transcriptional regulatory circuit controlled by TAL1 and its regulatory partners HEB, E2A, LMO1/2, GATA3, and RUNX1. We show that TAL1 forms a positive interconnected autoregulatory loop with GATA3 and RUNX1 and that the TAL1 complex directly activates the MYB oncogene, forming a positive feed-forward regulatory loop that reinforces and stabilizes the TAL1-regulated oncogenic program. One of the critical downstream targets in this circuitry is the TRIB2 gene, which is oppositely regulated by TAL1 and E2A/HEB and is essential for the survival of T-ALL cells.

Source URL: <http://www.cirm.ca.gov/about-cirm/publications/core-transcriptional-regulatory-circuit-controlled-tal1-complex-human-t-cell>